

- 1 -

<110> Asundi, Vinod
Ford, John E.
Drmanac, Radoje T.
Liu, Chenghua
Tang, Y. Tom
Yamasaki, Vicky
Yeung, George
Zhang, Jie
Zhou, Ping

<120> EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS

<130> 28110/36737

<150> US 09/620,312

<151> 2000-07-19

<150> US 09/363,316

<151> 1999-07-28

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<221> misc feature

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<223> n = A, T, C or G

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gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt 96
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
20 25 30

cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga 144
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
35 40 45

atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc 192
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
50 55 60

tac	aag	tgc	ttt	tgc	ctc	agt	ggc	cac	atg	ctc	atg	cca	gat	gct	acg	240
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	
65					70					75					80	

tgt	gtg	aac	tcn	agg	aca	tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	288
Cys	Val	Asn	Xaa	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	
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Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala	Thr	Cys	Glu	Pro	
1				5					10					15		
gga	tgt	aag	ttt	ggc	gag	tgc	gtg	gga	cca	aac	aaa	tgc	aga	tgc	ttt	96
Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	
			20					25					30			
cca	gga	tac	acc	ggg	aaa	acc	tgc	agt	caa	gat	gtg	aat	gag	tgt	gga	144
Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	
		35					40					45				
atg	aaa	ccc	cgg	cca	tgc	caa	cac	aga	tgt	gtg	aat	aca	cac	gga	agc	192
Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	
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tac	aag	tgc	ttt	tgc	ctc	agt	ggc	cac	atg	ctc	atg	cca	gat	gct	acg	240
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	
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tgt	gtg	aac	tcn	agg	aca	tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	288
Cys	Val	Asn	Xaa	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	
				85					90					95		
gaa	gac	aca	gaa	gaa	ggg	cca	cag	tgc	ctg	tgt	cca	tcc	tca	gga	ctc	336
Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	
			100					105					110			
cgc	ctg	gcc	cca	aat	gga	aga	gac	tgt	cta	gat	att	gat	gaa	tgt	gcc	384
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	
		115					120					125				
tct	ggc	aaa	gtc	atc	tgt	ccc	tac	aat	cga	aga	tgt	gtg	aac	aca	ttt	432
Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
	130					135					140					
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Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	
145					150					155					160	
agt	gga	cga	tat	gac	tgt	ata	gat	ata	aat	gaa	tgt	act	atg	gat	agc	528
Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	
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cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc	576
His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe	
180 185 190	
aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct	624
Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser	
195 200 205	
gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc	672
Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr	
210 215 220	
atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa	720
Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys	
225 230 235 240	
aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct	768
Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro	
245 250 255	
acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc	816
Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser	
260 265 270	
aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg	864
Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met	
275 280 285	
aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat	912
Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn	
290 295 300	
gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtg	960
Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val	
305 310 315 320	
aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta	1008
Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu	
325 330 335	
act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc	1056
Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser	
340 345 350	
ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt	1104
Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe	
355 360 365	
gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca	1152
Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala	
370 375 380	
gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt	1200
Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu	
385 390 395 400	
ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat	1248
Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp	
405 410 415	
tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa	1296
Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys	
420 425 430	

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Ile Leu Lys Leu Leu Ala Glu Lys Leu
530 535

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ggaggcggcg	gcttagctgc	tacgggg	tcc	ggccggcgcc	ctccc	gaggg	gggctcagga	180
ggaggaagga	ggacccgtgc	gaga	atg	cct	ctg	ccc	tgg agc ctt gcg ctc	231
			Met	Pro	Leu	Pro	Trp Ser Leu Ala Leu	
			1				5	
ccg	ctg	ctg	ctc	ccc	tgg	gtg	gca ggt ggt ttc ggg aac gcg gcc agt	279
Pro	Leu	Leu	Leu	Pro	Trp	Val	Ala Gly Gly Phe Gly Asn Ala Ala Ser	
	10				15		20	25
gca	agg	cat	cac	ggg	ttg	tta	gca tgc gca cgt cag cct ggg gtc tgt	327
Ala	Arg	His	His	Gly	Leu	Leu	Ala Ser Ala Arg Gln Pro Gly Val Cys	
				30			35	40
cac	tat	gga	act	aaa	ctg	gcc	tgc tgc tac ggc tgg aga aga aac agc	375
His	Tyr	Gly	Thr	Lys	Leu	Ala	Cys Cys Tyr Gly Trp Arg Arg Asn Ser	
			45				50	55
aag	gga	gtc	tgt	gaa	gct	aca	tgc gaa cct gga tgt aag ttt ggt gag	423
Lys	Gly	Val	Cys	Glu	Ala	Thr	Cys Glu Pro Gly Cys Lys Phe Gly Glu	
		60					65	70
tgc	gtg	gga	cca	aac	aaa	tgc	aga tgc ttt cca gga tac acc ggg aaa	471
Cys	Val	Gly	Pro	Asn	Lys	Cys	Arg Cys Phe Pro Gly Tyr Thr Gly Lys	
	75					80		85
acc	tgc	agt	caa	gat	gtg	aat	gag tgt gga atg aaa ccc cgg cca tgc	519
Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu Cys Gly Met Lys Pro Arg Pro Cys	
	90				95		100	105
caa	cac	aga	tgt	gtg	aat	aca	cac gga agc tac aag tgc ttt tgc ctc	567
Gln	His	Arg	Cys	Val	Asn	Thr	His Gly Ser Tyr Lys Cys Phe Cys Leu	
				110			115	120
agt	ggc	cac	atg	ctc	atg	cca	gat gct acg tgt gtg aac tct agg aca	615
Ser	Gly	His	Met	Leu	Met	Pro	Asp Ala Thr Cys Val Asn Ser Arg Thr	
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tgt	gcc	atg	ata	aac	tgt	cag	tat agc tgt gaa gac aca gaa gaa ggg	663
Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr Ser Cys Glu Asp Thr Glu Glu Gly	
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cca	cag	tgc	ctg	tgt	cca	tcc	tca gga ctc cgc ctg gcc cca aat gga	711
Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser Gly Leu Arg Leu Ala Pro Asn Gly	
	155					160		165
aga	gac	tgt	cta	gat	att	gat	gaa tgt gcc tct ggt aaa gtc atc tgt	759
Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu Cys Ala Ser Gly Lys Val Ile Cys	
	170				175		180	185
ccc	tac	aat	cga	aga	tgt	gtg	aac aca ttt gga agc tac tac tgc aaa	807
Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn Thr Phe Gly Ser Tyr Tyr Cys Lys	
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tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt	855
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys	
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ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat	903
Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His	
220 225 230	
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag	951
Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln	
235 240 245	
gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct	999
Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser	
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gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag	1047
Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys	
270 275 280	
aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa	1095
Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys	
285 290 295	
aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg	1143
Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu	
300 305 310	
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat	1191
Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His	
315 320 325	
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat	1239
Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp	
330 335 340 345	
gag aaa aga gaa gag aaa gcc ctg aag aat gac wta gag gag cga agc	1287
Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Xaa Glu Glu Arg Ser	
350 355 360	
ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc	1335
Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe	
365 370 375	
ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat	1383
Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His	
380 385 390	
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt	1431
Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys	
395 400 405	
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat	1479
Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp	
410 415 420 425	
cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt	1527
Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly	
430 435 440	
cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa	1575
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<213> Homo sapiens

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Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	Leu	Leu
			20					25					30		
Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	Lys	Leu	Ala
		35				40					45				
Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala	Thr
	50				55					60					
Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys
65				70					75					80	
Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn
			85					90					95		
Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr
			100				105					110			

His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro
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Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln
	130					135				140					
Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser
145				150					155					160	
Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp
			165					170						175	
Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val
		180						185				190			
Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu
	195						200				205				
Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr
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225				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu
			245					250					255		
Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala
			260				265						270		
Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn
		275				280						285			
Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr
	290				295					300					
Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu
305				310					315					320	
Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu
			325					330					335		
Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala
		340					345					350			
Leu	Lys	Asn	Asp	Xaa	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe
	355					360					365				
Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg
	370				375					380					
Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val
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Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	Glu
			405					410					415		
Asp	Asp	Phe	Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	Phe
		420					425					430			
Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	His	Lys	Lys	Asp	Ile	Gly	Arg
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Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu
450					455					460					
Leu	Phe	Asp	Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val
465				470					475					480	
Phe	Val	Lys	Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser
			485				490						495		
Glu	Asp	Glu	Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	Thr
		500					505					510			
Asp	Ala	Thr	Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	Lys
	515					520					525				
Thr	Gly	Glu	Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	Cys
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 <213> Drosophila Melanogaster

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 35 40 45
 Asp Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
 50 55 60
 Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
 65 70 75 80
 Arg Leu Ala Pro Asn Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys
 85 90 95
 Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys
 100 105 110
 Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Ile Asn Glu
 115 120 125
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<223> Xaa = Any Amino Acid

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Xaa	Cys	Xaa	Asn	Thr	Val	Gly	Ser	Tyr	Xaa	Cys	Arg	Cys	Arg	Pro	Gly
			20					25					30		
Trp	Xaa	Pro	Xaa	Pro	Gly	Xaa	Pro	Asn	Xaa	Xaa	Xaa	Asp			
		35					40					45			

<213> Mammalian

<223> Xaa = Any Amino Acid

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			20					25					30		
Cys	Val	Val	Gly	Tyr	Ile	Xaa	Xaa	Xaa	Gly	Glu	Arg	Xaa	Xaa	Cys	Gln
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<213> Artificial Sequence

<223> Gene-specific PCR primer 10244-52

21

<213> Artificial Sequence

<223> Gene-specific PCR primer 10244-51

21

<213> Artificial Sequence

$\langle 220 \rangle$

<400> 14

21

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<212> DNA

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<223> Vector primer SP6

<400> 15

22

<210> 16

 $\langle 211 \rangle$ 21

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Gene-specific PCR primer 10244-A

<400> 16

21

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Gene-specific PCR primer 10244-B

<400> 17

21

<210> 18

<211> 502

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1) ... (502)

<223> Xaa = Any Amino Acid

<400> 18

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Pro	Gly	Tyr 35	Thr	Gly	Lys	Thr	Cys 40	Ser	Gln	Asp	Val	Asn 45	Glu	Cys	Gly
Met	Lys 50	Pro	Arg	Pro	Cys	Gln 55	His	Arg	Cys	Val	Asn 60	Thr	His	Gly	Ser
Tyr 65	Lys	Cys	Phe	Cys	Leu 70	Ser	Gly	His	Met	Leu 75	Met	Pro	Asp	Ala	Thr 80
Cys	Val	Asn	Ser	Arg 85	Thr	Cys	Ala	Met	Ile 90	Asn	Cys	Gln	Tyr	Ser 95	Cys
Glu	Asp	Thr	Glu 100	Gly	Gly	Pro	Gln	Cys 105	Leu	Cys	Pro	Ser	Ser 110	Gly	Leu

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<212> DNA
<213> Artificial Sequence
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21

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<223> Description of Artificial Sequence: primer

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<211> 20
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<220>
<223> Description of Artificial Sequence: primer

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<210> 22
<211> 20
<212> DNA
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<220>
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<211> 2365
<212> DNA
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ggagggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccgaggg gggctcagga 180
ggaggaagga ggacccgtgc gaga atg cct ctg ccc tgg agc ctt gcg ctc      231
                        Met Pro Leu Pro Trp Ser Leu Ala Leu
                        1                      5

ccg ctg ctg ctc tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt      279
Pro Leu Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser
10                      15                      20                      25

gca agg cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt      327
Ala Arg His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys
                        30                      35                      40

cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc      375
His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser
                        45                      50                      55

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00ETOT"09828950

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Cys	Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	
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acc	tgc	agt	caa	gat	gtg	aat	gag	tgt	gga	atg	aaa	ccc	cgg	cca	tgc	519
Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
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Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	
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Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	
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Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	
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Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	
	155					160					165					
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Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	
				190					195					200		
tgt	cac	att	ggg	ttc	gaa	ctg	caa	tat	atc	agt	gga	cga	tat	gac	tgt	855
Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	
			205					210					215			
ata	gat	ata	aat	gaa	tgt	act	atg	gat	agc	cat	acg	tgc	agc	cac	cat	903
Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	
		220					225					230				
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Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	
	235					240					245					
gga	tat	aaa	ggc	aat	gga	ctt	cgg	tgt	tct	gct	atc	cct	gaa	aat	tct	999
Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	
	250				255					260					265	
gtg	aag	gaa	gtc	ctc	aga	gca	cct	ggg	acc	atc	aaa	gac	aga	atc	aag	1047
Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	
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Lys	Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	
			285					290					295			
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Asn	Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	
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Gln	Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	
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Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	Asp	Ile	Glu	Glu	Arg	Ser	
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Gly	Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	
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aaa	gat	tta	aat	atc	tcg	gtt	gac	tgc	agc	ttc	aat	cat	ggg	atc	tgt	1431
Lys	Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	
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gac	tgg	aaa	cag	gat	aga	gaa	gat	gat	ttt	gac	tgg	aat	cct	gct	gat	1479
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	410				415					420					425	
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Arg	Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	
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cac	aag	aaa	gac	att	ggc	cga	ttg	aaa	ctt	ctc	cta	cct	gac	ctg	caa	1575
His	Lys	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	
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ccc	caa	agc	aac	ttc	tgt	ttg	ctc	ttt	gat	tac	cgg	ctg	gcc	gga	gac	1623
Pro	Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp	Tyr	Arg	Leu	Ala	Gly	Asp	
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Lys	Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys	Asn	Ser	Asn	Asn	Ala	Leu	
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Ala	Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu	Lys	Trp	Lys	Thr	Gly	Lys	
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Ile	Gln	Leu	Tyr	Gln	Gly	Thr	Asp	Ala	Thr	Lys	Ser	Ile	Ile	Phe	Glu	
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Ala	Glu	Arg	Gly	Lys	Gly	Lys	Thr	Gly	Glu	Ile	Ala	Val	Asp	Gly	Val	
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satcatagga	cctctggcat	tttaaaatta	ctaagctgaa	aaattgtaat	gtaccaacag	1983										

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Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	Lys	Leu	Ala
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Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala	Thr
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Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys
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Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn
				85					90					95	
Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr
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His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro
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Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln
	130						135				140				
Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser
145				150						155				160	
Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp
			165					170					175		
Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val
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Asn	Thr	Phe 195	Gly	Ser	Tyr	Tyr	Cys 200	Lys	Cys	His	Ile	Gly 205	Phe	Glu	Leu
Gln	Tyr 210	Ile	Ser	Gly	Arg	Tyr 215	Asp	Cys	Ile	Asp	Ile 220	Asn	Glu	Cys	Thr
Met 225	Asp	Ser	His	Thr	Cys 230	Ser	His	His	Ala	Asn 235	Cys	Phe	Asn	Thr	Gln 240
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Arg	Cys	Ser	Ala 260	Ile	Pro	Glu	Asn 265	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala
Pro	Gly	Thr 275	Ile	Lys	Asp	Arg	Ile 280	Lys	Lys	Leu	Leu	Ala 285	His	Lys	Asn
Ser	Met 290	Lys	Lys	Lys	Ala	Lys 295	Ile	Lys	Asn	Val	Thr 300	Pro	Glu	Pro	Thr
Arg 305	Thr	Pro	Thr	Pro	Lys 310	Val	Asn	Leu	Gln	Pro 315	Phe	Asn	Tyr	Glu	Glu 320
Ile	Val	Ser	Arg	Gly 325	Gly	Asn	Ser	His	Gly 330	Gly	Lys	Lys	Gly	Asn 335	Glu
Glu	Lys	Met	Lys 340	Glu	Gly	Leu	Glu	Asp 345	Glu	Lys	Arg	Glu	Glu 350	Lys	Ala
Leu	Lys	Asn 355	Asp	Ile	Glu	Glu	Arg 360	Ser	Leu	Arg	Gly	Asp 365	Val	Phe	Phe
Pro	Lys 370	Val	Asn	Glu	Ala	Gly 375	Glu	Phe	Gly	Leu	Ile 380	Leu	Val	Gln	Arg
Lys 385	Ala	Leu	Thr	Ser	Lys 390	Leu	Glu	His	Lys	Asp 395	Leu	Asn	Ile	Ser	Val 400
Asp	Cys	Ser	Phe	Asn 405	His	Gly	Ile	Cys	Asp 410	Trp	Lys	Gln	Asp	Arg 415	Glu
Asp	Asp	Phe	Asp 420	Trp	Asn	Pro	Ala	Asp 425	Arg	Asp	Asn	Ala	Ile 430	Gly	Phe
Tyr	Met	Ala 435	Val	Pro	Ala	Leu	Ala 440	Gly	His	Lys	Lys	Asp 445	Ile	Gly	Arg
Leu	Lys 450	Leu	Leu	Leu	Pro	Asp 455	Leu	Gln	Pro	Gln	Ser 460	Asn	Phe	Cys	Leu
Leu 465	Phe	Asp	Tyr	Arg	Leu 470	Ala	Gly	Asp	Lys	Val 475	Gly	Lys	Leu	Arg	Val 480
Phe	Val	Lys	Asn	Ser 485	Asn	Asn	Ala	Leu	Ala 490	Trp	Glu	Lys	Thr	Thr 495	Ser
Glu	Asp	Glu	Lys 500	Trp	Lys	Thr	Gly	Lys 505	Ile	Gln	Leu	Tyr	Gln 510	Gly	Thr
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Pro Asp Ser Leu Leu Ser Val Asp Asp
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<220>
<223> Description of Artificial Sequence: Primer

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<211> 30
<212> DNA
<213> Artificial Sequence
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<210> 27
<211> 2360
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<223> n = a,t,c or g
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cgtgcgaga		atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc													228
		Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu													
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tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg ggt tct															276
Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg Gly Ser															
14				19					24				29		

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Val	Cys	His	Tyr	Gly	Thr	Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	
46					51					56					61	
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62					67					72					77	
ggg	gag	tgc	gtg	gga	cca	aac	aaa	tgc	aga	tgc	ttt	cca	gga	tac	acc	468
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78					83					88					93	
ggg	aaa	acc	tgc	agt	caa	gat	gtg	aat	gag	tgt	gga	atg	aaa	ccc	cgg	516
Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	
94					99					104					109	
cca	tgc	caa	cac	aga	tgt	gtg	aat	aca	cac	gga	agc	tac	aag	tgc	ttt	564
Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	
110					115					120					125	
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Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
126					131					136					141	
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Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	
142					147					152					157	
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Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	
158					163					168					173	
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Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	
174					179					184					189	
atc	tgt	ccc	tac	aat	cga	aga	tgt	gtg	aac	aca	ttt	gga	agc	tac	tac	804
Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	
190					195					200					205	
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Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	
206					211					216					221	
gac	tgt	ata	gat	ata	aat	gaa	tgt	act	atg	gat	agc	cat	acg	tgc	agc	900
Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	
222					227					232					237	
cac	cat	gcc	aat	tgc	ttc	aat	acc	caa	ggg	tcc	ttc	aag	tgt	aaa	tgc	948
His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	
238					243					248					253	
aag	cag	gga	tat	aaa	ggc	aat	gga	ctt	cgg	tgt	tct	gct	atc	cct	gaa	996
Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	
254					259					264					269	
aat	tct	gtg	aag	gaa	gtc	ctc	aga	gca	cct	ggg	acc	atc	aaa	gac	aga	1044
Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	
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542                      547                      552                      557

gat gac tga atgttac tatctttata ttgactttg tatgtcagtt ccttggtttt      1916
Asp Asp  *
558

tttgatattg catcatagga cctctggcat tttagaatta ctagctgaaa aattgtaatg      1976

taccaacaga aatattattg taagatgcct ttcttgtata agatatgcca atatttgctt      2036

taaatatcat atcactgtat cttctcagtc atttctgaat ctttccacat tatattataa      2096

aatatggaaa tgtcagttta tctccctcc tcagtatatc tgatttgtat aagtaagttg      2156

atgagcttct ctctacaaca tttctagaaa atagaaaaaa aagcacagag aaatgtttaa      2216

ctgtttgact cttatgatac ttcttggaac ctatgacatc aaagatagac ttttgcctaa      2276

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His His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His
      35                      40                      45

Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys
      50                      55                      60

Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys
      65                      70                      75                      80

Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr
      85                      90                      95

Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln
      100                      105                      110

His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser
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Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys
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Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro
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Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg
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Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	195	200	205
His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	210	215	220
Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	225	230	235
Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	245	250	255
Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	260	265	270
Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	275	280	285
Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	290	295	300
Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	305	310	315
Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	325	330	335
Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	340	345	350
Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	Asp	Ile	Glu	Glu	Arg	Ser	Leu	355	360	365
Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	370	375	380
Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	385	390	395
Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	405	410	415
Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe	Asp	Trp	Asn	Pro	Ala	Asp	Arg	420	425	430
Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	His	435	440	445
Lys	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	Pro	450	455	460
Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp	Tyr	Arg	Leu	Ala	Gly	Asp	Lys	465	470	475
Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys	Asn	Ser	Asn	Asn	Ala	Leu	Ala	485	490	495
Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu	Lys	Trp	Lys	Thr	Gly	Lys	Ile	500	505	510

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Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala
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 Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu
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 ctgctacggg gtccgggccg ggcgcctccc gaggggggct caggaggagg aaggaggacc 180
 cgtgcgaga atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc 228
 Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu
 1 5 10
 tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg cat cat 276
 Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His
 14 19 24 29
 cac ggg ttg tta gca tgc gca cgt cag cct ggg gtc tgt cac tat gga 324
 His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly
 30 35 40 45
 act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc aag gga gtc 372
 Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val
 46 51 56 61
 tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag tgc gtg gga 420
 Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly
 62 67 72 77
 cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa acc tgc agt 468
 Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser
 78 83 88 93
 caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc caa cac aga 516
 Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg
 94 99 104 109
 tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc agt ggc cac 564
 Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His
 110 115 120 125

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Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	
126					131					136					141	
ata	aac	tgt	cag	tac	agc	tgt	gaa	gac	aca	gaa	gaa	ggg	cca	cag	tgc	660
Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	
142					147					152					157	
ctg	tgt	cca	tcc	tca	gga	ctc	cgc	ctg	gcc	cca	aat	gga	aga	gac	tgt	708
Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	
158					163					168					173	
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Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	
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cga	aga	tgt	gtg	aac	aca	ttt	gga	agc	tac	tac	tgc	aaa	tgt	cac	att	804
Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	
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Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	
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Ala	His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
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Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	
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Asn	Tyr	Glu	Glu	Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	
318					323					328					333	
aaa	ggg	aat	gaa	gag	aaa	atg	aaa	gag	ggg	ctt	gag	gat	gag	aaa	aga	1236
Lys	Gly	Asn	Glu	Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	
334					339					344					349	
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Glu	Glu	Lys	Ala	Leu	Lys	Asn	Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	
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Asp	Val	Phe	Phe	Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	
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Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys	
398 403 408 413	
cag gat aga gaa gat gat ttt gac tgg aat cct gct gat cga gat aat	1476
Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn	
414 419 424 429	
gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt cac aag aaa	1524
Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys	
430 435 440 445	
gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa ccc caa agc	1572
Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser	
446 451 456 461	
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462 467 472 477	
aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg gca tgg gag	1668
Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu	
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Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu	
494 499 504 509	
tat caa gga act gat gct acc aaa agc atc att ttt gaa gca gaa cgt	1764
Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg	
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Leu	Ala	Ser 35	Ala	Arg	Gln	Pro	Gly 40	Val	Cys	His	Tyr	Gly 45	Thr	Lys	Leu
Ala	Cys 50	Cys	Tyr	Gly	Trp	Arg 55	Arg	Asn	Ser	Lys	Gly 60	Val	Cys	Glu	Ala
Thr 65	Cys	Glu	Pro	Gly	Cys 70	Lys	Phe	Gly	Glu	Cys 75	Val	Gly	Pro	Asn	Lys 80
Cys	Arg	Cys	Phe	Pro 85	Gly	Tyr	Thr	Gly	Lys 90	Thr	Cys	Ser	Gln	Asp 95	Val
Asn	Glu	Cys	Gly 100	Met	Lys	Pro	Arg	Pro 105	Cys	Gln	His	Arg	Cys 110	Val	Asn
Thr	His 115	Gly	Ser	Tyr	Lys	Cys	Phe 120	Cys	Leu	Ser	Gly	His 125	Met	Leu	Met
Pro	Asp 130	Ala	Thr	Cys	Val	Asn 135	Ser	Arg	Thr	Cys	Ala 140	Met	Ile	Asn	Cys
Gln 145	Tyr	Ser	Cys	Glu	Asp 150	Thr	Glu	Glu	Gly	Pro 155	Gln	Cys	Leu	Cys	Pro 160
Ser	Ser	Gly	Leu	Arg 165	Leu	Ala	Pro	Asn	Gly 170	Arg	Asp	Cys	Leu	Asp 175	Ile
Asp	Glu	Cys	Ala 180	Ser	Gly	Lys	Val	Ile 185	Cys	Pro	Tyr	Asn	Arg 190	Arg	Cys
Val	Asn 195	Thr	Phe	Gly	Ser	Tyr	Tyr 200	Cys	Lys	Cys	His	Ile 205	Gly	Phe	Glu
Leu	Gln 210	Tyr	Ile	Ser	Gly	Arg 215	Tyr	Asp	Cys	Ile	Asp 220	Ile	Asn	Glu	Cys
Thr 225	Met	Asp	Ser	His	Thr 230	Cys	Ser	His	His	Ala 235	Asn	Cys	Phe	Asn	Thr 240
Gln	Gly	Ser	Phe	Lys 245	Cys	Lys	Cys	Lys	Gln 250	Gly	Tyr	Lys	Gly	Asn 255	Gly
Leu	Arg	Cys	Ser	Ala 260	Ile	Pro	Glu	Asn 265	Ser	Val	Lys	Glu	Val 270	Leu	Arg
Ala	Pro 275	Gly	Thr	Ile	Lys	Asp	Arg 280	Ile	Lys	Lys	Leu	Leu 285	Ala	His	Lys

Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro
290 295 300

Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu
305 310 315 320

Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn
325 330 335

Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys
340 345 350

Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe
355 360 365

Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln
370 375 380

Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser
385 390 395 400

Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg
405 410 415

Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly
420 425 430

Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly
435 440 445

Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys
450 455 460

Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg
465 470 475 480

Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr
485 490 495

Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly
500 505 510

Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly
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Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu
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Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg
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cat cac ggg ttg tta gca tgc gca cgt cag cct ggg gtc tgt cac tat 386
His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr
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Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly
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Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val
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Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys
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Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His
95 100 105
aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc agt ggc 626
Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly
110 115 120
cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca tgt gcc 674
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Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln
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Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp
160 165 170
tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt ccc tac 818
Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr
175 180 185
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Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp
205 210 215

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Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn	
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Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr	
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Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys	
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Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu	
270 275 280	
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Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val	
285 290 295	
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Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro	
300 305 310 315	
ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat gga ggt	1250
Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly	
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Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys	
335 340 345	
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Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg	
350 355 360	
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Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu	
365 370 375	
att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat aaa gca	1442
Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Ala	
380 385 390 395	
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Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp	
400 405 410	
tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat cga	1538
Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg	
415 420 425	
gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt cac	1586
Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His	
430 435 440	
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Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro	
445 450 455	
caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac aaa	1682
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Met	Pro	Leu	Pro	Trp	Ser	Leu	Ala	Leu	Pro	Leu	Leu	Leu	Ser	Trp	Val
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Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	Leu	Leu
			20					25					30		
Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	Lys	Leu	Ala
		35					40					45			
Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala	Thr
50						55					60				
Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys
65					70					75					80
Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn
				85					90					95	

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Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly
435 440 445

Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys
450 455 460

Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg
465 470 475 480

Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr
485 490 495

Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly
500 505 510

Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly
515 520 525

Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu
530 535 540

Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
545 550

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